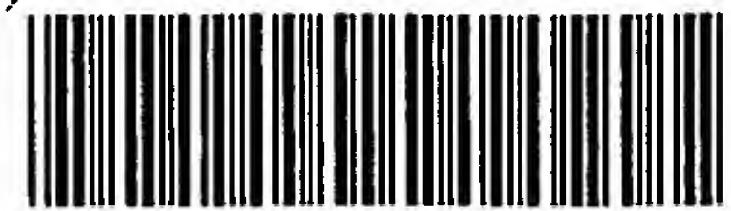


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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/940,925A

DATE: 06/21/2002
TIME: 12:20:02

Input Set : A:\Seqsub2.app
Output Set: N:\CRF3\06212002\I940925A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: BROW, MARY ANN D.
7 LYAMICHEV, VICTOR I.
8 OLIVE, DAVID M.

10 (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
11 PATHOGENS

13 (iii) NUMBER OF SEQUENCES: 165

15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: MEDLEN & CARROLL
17 (B) STREET: 220 MONTGOMERY STREET, SUITE 2200
18 (C) CITY: SAN FRANCISCO
19 (D) STATE: CALIFORNIA
20 (E) COUNTRY: UNITED STATES OF AMERICA
21 (F) ZIP: 94104

23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US/09/940,925A
31 (B) FILING DATE: 10-Jun-2002
32 (C) CLASSIFICATION:
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: CARROLL, PETER G.
36 (B) REGISTRATION NUMBER: 32,837
37 (C) REFERENCE/DOCKET NUMBER: FORS-01756

39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (415) 705-8410
41 (B) TELEFAX: (415) 397-8338

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:
47 (A) LENGTH: 2506 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 ATGAGGGGGA TGCTGCCCTT CTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
60 CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
62 GTGCAGGCAG TCTACGGCTT CGCCAAGAGC CTCCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
64 GCGGTGATCG TGGTCTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/940,925A

DATE: 06/21/2002
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66	TACAAGGCGG	GCCGGGCC	CACGCCGGAG	GA	CTTTCCC	GGCAACTCGC	CCTCATCAAG	300		
68	GAGCTGGTGG	ACCTCCTGGG	GCTGGCGCGC	CTCGAGGTCC	CGGGCTACGA	GGCGGACGAC	360			
70	GTCCTGGCCA	GCCTGGCAA	GAAGGCGGAA	AAGGAGGGCT	ACGAGGTCCG	CATCCTCAC	420			
72	GCCGACAAAG	ACCTTACCA	GCTCCTTCC	GACCGCATCC	ACGTCC	CCCCGAGGGG	480			
74	TACCTCATCA	CCCCGGCCTG	GCTTGGGAA	AAGTACGGCC	TGAGGCCGA	CCAGTGGGCC	540			
76	GA	CTACC	GGG	CCCTGACCGG	GGACGAGTCC	GACAACCTTC	CCGGGGTCAA	600		
78	GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660			
80	CTGGACCGGC	TGAAGCCC	G	CATCCGGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720		
82	CTCTCCTGGG	ACCTGGCAA	GGTGC	GACC	TGGAGGTGGA	CTTCGCCAAA	780			
84	AGGCGGGAGC	CCGACCGGG	GAGGCTTAGG	GCCTTCTGG	AGAGGCTTGA	TTTGGCAGC	840			
86	CTCCTCCACG	AGTTCGGC	TCTGGAAAGC	CCC	AGGCCC	TGGAGGAGGC	CCCCTGGCCC	900		
88	CCGCCGGAAG	GGGCCTTCGT	GGGCTTG	CTTCCC	GCA	AGGAGCCAT	GTGGGCCGAT	960		
90	CTTCTGGCCC	TGGCGCC	GC	CAGGGGGG	CGGGTCCACC	GGGCC	GCCTTATAAA	1020		
92	GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGG	CTTCTG	CC	AAGACCTGAG	CGTTCTGGCC	1080		
94	CTGAGGGAAAG	GCCTTGGC	CCC	GCC	GAC	TGCTCCTCGC	CTACCTCCTG	1140		
96	GACCCTCCA	ACACCACCCC	CGAGGGGG	TG	CCGGCG	ACGGCGGGG	GTGGACGGAG	1200		
98	GAGGCGGGGG	AGCGGGCC	GC	CCTTCCGAG	AGGCTTT	CCAACCTGTG	GGGGAGGCTT	1260		
100	GAGGGGGAGG	AGAGGCTC	CT	GGCTT	TAC	CGGGAGGTGG	AGAGGCCCCT	1320		
102	CTGGCCCACA	TGGAGG	CCAC	GGGGT	GC	CTGGAC	GTGG	1380		
104	CTGGAGGTGG	CCGAGG	GAGAT	CGCC	CGC	GAGG	TCTTCCG	1440		
106	CCCTTCAACC	TCAACT	CCCG	GGACC	AGCTG	GAAAGGGTCC	TCTTGTACGA	1500		
108	CCGCCATCG	GCAAGACGGA	GAAGAC	CCGG	AAGCG	CTCCA	CCAGCGCC	1560		
110	GCCCTCCGCG	AGGCCCACCC	CATCG	TGGAG	AAGATC	CTGC	AGTACCGGG	1620		
112	CTGAAGAGCA	CCTACATTGA	CCC	CTGCC	GAC	CTCATCC	ACCC	AGGAC	GGCCG	1680
114	CACACCGCT	TCAACCAGAC	GGCC	ACGG	CGAGG	TAAGTAG	CTCG	CGAT	CCCAAC	1740
116	CTCCAGAAC	TCCCCGTCC	CAC	CCG	GCTT	GGG	CAGAGGA	TCC	GCCGG	1800
118	GAGGAGGGT	GGCTATTGGT	GGC	CCTGG	GAC	TATAGCC	AGA	GCTC	AG	1860
120	CACCTCTCCG	GCGACGAGAA	CCTG	ATCCG	GG	GTCTT	CCAGG	AGGG	CGGG	1920
122	GAGACCGCCA	GCTGGATGTT	CGG	CGT	CCCC	CGGG	AGGGCC	TGG	ACCC	1980
124	GCGGCCAAGA	CCATCAACTT	CGGG	GTCC	TACGG	CATGT	CGG	CCC	ACCG	2040
126	GAGCTAGCCA	TCCCTTACGA	GGAGG	CCC	AG	GCCT	CATTG	AGCG	CTACTT	2100
128	CCCAAGGTGC	GGGCCTGGAT	TGAGA	AGACC	CTGG	AGGAGG	GCAGG	AGGCG	GGGGTACGTG	2160
130	GAGACCCTCT	TCGGCCGCG	CCG	CTACGTG	CCAGAC	CTAG	AGG	CCC	GGGT	2220
132	CGGGAGGCGG	CCGAGCGCAT	GGC	CTTCAAC	ATG	CCC	GTCC	AGGG	CACCGC	2280
134	ATGAAGCTGG	CTATGGTGAA	GCT	CTTCCCC	AGG	CTGG	AGG	AAAT	GGGGC	2340
136	CTTCAGGTCC	ACGACGAGCT	GGT	CCTCG	GAG	GCCC	AAAAG	AGAGG	GGGA	2400
138	CGGCTGGCCA	AGGAGGTCA	GGAGGGGG	TAT	CCC	CTGG	CCGT	CCCC	CT	2460
140	GTGGGGATAG	GGGAGGACTG	GCT	CTCCG	CC	AAGGAGT	GAT	ACC	AC	2506
142	(2)	INFORMATION FOR SEQ ID NO: 2:								
144	(i)	SEQUENCE CHARACTERISTICS:								
145	(A)	LENGTH: 2496 base pairs								
146	(B)	TYPE: nucleic acid								
147	(C)	STRANDEDNESS: double								
148	(D)	TOPOLOGY: linear								
150	(ii)	MOLECULE TYPE: DNA (genomic)								
154	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:								
156	ATGGCGATGC	TTCCC	CTT	TGAGCC	AAA	GGCGCGT	GC	CC	AC	60
158	CTGGC	CTT	AC	GCAC	CTT	GG	CC	CT	AC	120
160	CAGGCGGT	CT	ACGG	CTT	CGC	CAA	AA	AGG	CC	180

RAW SEQUENCE LISTING
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Input Set : A:\Seqsub2.app
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162	GTGGTGGTGG	TCTTGACGC	CAAGGCC	TCCTTCCGCC	ACGAGGC	CGAGGC	TAC	240		
164	AAGGC	GGGGC	CCC	GAGGAC	TTTCCCCG	AGCTGG	CCT	300		
166	TTGGTGGACC	TCCTAGGC	TGTGCGG	GAGGTTCC	GCTTGAGG	GGACGAC	TG	360		
168	CTGGCCACCC	TGGCCAAGCG	GGCGGAA	GAGGGGTACG	AGGTGCG	CCTCA	TGCC	420		
170	GACCGCGACC	TCTACCAGCT	CCTTCCGGAG	CGCATCGCC	TCCTCCACCC	TGAGGGGTAC	480			
172	CTGATCACCC	CGGC	GTGG	TTACGAGAAG	TACGGC	GCCC	GGAGCA	540		
174	TACCGGGCCC	TGGCGGGGGA	CCCCTCGG	AACATCCC	GGGTGAAGGG	CATCG	GGGAG	600		
176	AAGACCGCCC	AGAGGCTCAT	CCCG	GAGTGG	GGGAGCCTGG	AAAAC	CTCTT	CCAGCAC	660	
178	GACCAGGTGA	AGCC	CTCC	GAGAAG	CTCCAGGCG	GCATGG	GAGGC	CCTGG	720	
180	TCCC	GGAAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCC	AGGTGG	ACTT	CGGGAGGCG	780	
182	CGCACACCC	AC	TGGAGGG	TCTGCGGG	TTTTGGAGC	GGTTGG	AGTT	TGGAAGC	840	
184	CTCCACGAGT	TCGGC	CTCC	GGAGGGCG	AAGGCGG	AGGAGG	CCCC	CTGG	900	
186	CCGGAAGGGG	CTTTT	TGGG	CTTTCC	TCCC	GTCCC	AGCC	ATGTG	960	
188	CTGGCC	CTGG	GGCG	GGAGGGCG	CTCC	CATCGG	CACA	AGACCC	1020	
190	CTGAGGGACC	TTAAGGGG	GCGGG	GAATC	CTGGC	CAAGG	ACCTGG	CGGT	1080	
192	CGGGAGGGCC	TGGAC	CTCTT	CCCAGAGG	GACCC	CATGC	TCCTG	GCC	1140	
194	CCCTCCAACA	CCAC	CCCTGA	GGGGTGG	CGCG	TTACG	GGGGG	GAGTG	1200	
196	CGGGGGGAGA	GGG	CCCTC	GGCG	CTCTT	CCAGA	CCCTAA	AGGA	1260	
198	GGAGAAGAAC	GCCTG	TTTG	GCTTACG	GAGG	TGGAGA	AGCCG	CTTTC	1320	
200	GCCCGG	ATGG	AGGCC	ACGGG	GGTCC	GGCTG	GACG	TGGC	1380	
202	GAGGTGGAGG	CGGAGG	TGCG	CCAG	CTGG	GAGG	TCT	TCCG	1440	
204	TTCAAC	CTCA	ACTCCC	GCGA	CCAG	CTGG	GGCTG	CCT	1500	
206	GCCATCGG	CA	AGACGG	GAGAA	GACGGG	GGCT	CCAC	AGGCA	1560	
208	CTGCGAGAGG	CCCAC	CCC	CAT	CGTGG	ACCC	GGAGC	T	1620	
210	AAGAACAC	CT	ACATAGAC	CCC	CCTG	CCACC	CCAAGAC	CCGG	1680	
212	ACCCG	CTTCA	ACCAGAC	GGC	CACCG	GGCAGG	CTT	CCAGCT	1740	
214	CAGAACAT	CC	CGT	CGC	AC	CCCT	CTGG	CGAG	1800	
216	GAGGG	CTGG	TGCT	GGGT	CTTG	ACTAC	AGCC	AGATTG	1860	
218	CTCT	CCGGG	ACGAGAAC	CT	CCGGG	TC	TTCA	GGAGG	1920	
220	ACCGC	CAGCT	GGAT	GTT	CGG	TTT	CCCC	GAAGGG	1980	
222	GCCAAGAC	CA	TCAACT	TCGG	GGT	GCTCT	GGC	ATGTCC	2040	
224	CTTCC	CAT	CC	TACGAG	GGC	GGT	GGC	TTCATTGAGC	2100	
226	AAGGTG	CGGG	CCTG	GATT	GGG	ACC	CTT	GACCTCAACG	2160	
228	ACC	CTT	CG	GCC	CCGG	CTAT	GAGG	CCC	GGGTGAA	2220
230	GAGGCG	GG	AGCG	CAT	GGC	CTTCA	ACAT	GG	GCAC	2280
232	AAGCTGG	CCA	TGGT	GGG	CTT	CCCC	CC	GGGAAC	2340	
234	CAGGTG	CACG	ACG	AGCTGG	CCT	CGAGG	CCC	AGGACC	2400	
236	TTGG	CCA	AGG	TCA	GGG	GTCT	GG	GGAGGT	2460	
238	GGC	CTGG	GGG	AGG	ACTGG	CTCC	GCCA	AG	2496	

240 (2) INFORMATION FOR SEQ ID NO: 3:

242 (i) SEQUENCE CHARACTERISTICS:

243 (A) LENGTH: 2504 base pairs

244 (B) TYPE: nucleic acid

245 (C) STRANDEDNESS: double

246 (D) TOPOLOGY: linear

248 (ii) MOLECULE TYPE: DNA (genomic)

252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

254 ATGGAGGCGA TGCTTCCGCT CTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGCCAC

256 CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG

60

120

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Input Set : A:\Seqsub2.app
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258	GTGCAGGCAG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTGAAGGA	GGACGGGTAC	180
260	AAGGCCGTCT	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGAG	240
262	GCCTACAAAGG	CGGGGAGGGC	CCCGACCCCC	GAGGACTTCC	CCCAGCAGCT	CGCCCTCATC	300
264	AAGGAGCTGG	TGGACCTCCT	GGGGTTTACC	CGCCTCGAGG	TCCCCGGCTA	CGAGGCGGAC	360
266	GACGTTCTCG	CCACCCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATTCTC	420
268	ACCGCCGACC	GCGACCTCTA	CCAACTCGTC	TCCGACCGCG	TCGCCGTCTT	CCACCCCGAG	480
270	GGCCACCTCA	TCACCCCGGA	GTGGCTTGG	GAGAAGTACG	GCCTCAGGCC	GGAGCAGTGG	540
272	GTGGACTTCC	GCGCCCTCGT	GGGGGACCCC	TCCGACAACC	TCCCCGGGT	CAAGGGCATT	600
274	GGGGAGAAGA	CCGCCCTCAA	GCTCCTCAAG	GAGTGGGAA	GCCTGGAAAA	CCTCCTCAAG	660
276	AACCTGGACC	GGGTAAAGCC	AGAAAACGTC	CGGGAGAAGA	TCAAGGCCA	CCTGGAAGAC	720
278	CTCAGGCTCT	CCTTGGAGCT	CTCCCGGGTG	CGCACCGACC	TCCCCCTGG	GGTGGACCTC	780
280	GCCCAGGGGC	GGGAGCCCGA	CCGGGAGGGG	CTTAGGGCCT	TCCTGGAGAG	GCTGGAGTTC	840
282	GGCAGCCTCC	TCCACGAGTT	CGGCCTCCTG	GAGGCCCCCG	CCCCCTGG	GGAGGCCCCC	900
284	TGGCCCCCGC	CGGAAGGGGC	CTTCGTGGGC	TCGTCCTCT	CCCGCCCCGA	GCCATGTGG	960
286	GCGGAGCTTA	AAGCCCTGGC	CGCCTGCAGG	GACGGCCGGG	TGCACCGGGC	AGCAGACCCC	1020
288	TTGGCGGGGC	TAAAGGACCT	CAAGGAGGTC	CGGGGCCTCC	TCGCCAAGGA	CCTGCCGT	1080
290	TTGGCCTCGA	GGGAGGGGCT	AGACCTCGTG	CCCAGGGACG	ACCCCATGCT	CCTCGCCTAC	1140
292	CTCCTGGACC	CCTCCAACAC	CACCCCGAG	GGGGTGGCGC	GGCGCTACGG	GGGGGAGTGG	1200
294	ACGGAGGACG	CCGCCCACCG	GGCCCTCCTC	TCGGAGAGGC	TCCATCGAA	CCTCCTTAAG	1260
296	CGCCTCGAGG	GGGAGGAGAA	GCTCCTTGG	CTCTACCACG	AGGTGGAAAA	GCCCCTCTCC	1320
298	CGGGTCCTGG	CCCACATGG	GGCCACCGGG	GTACGGCTGG	ACGTGGCCTA	CCTTCAGGCC	1380
300	CTTCCCTGG	AGCTTGCAGA	GGAGATCCGC	CGCCTCGAGG	AGGAGGTCTT	CCGCTTGGCG	1440
302	GGCCACCCCT	TCAACCTCAA	CTCCCGGGAC	CAGCTGGAAA	GGGTGCTCTT	TGACGAGCTT	1500
304	AGGCTTCCCG	CCTTGGGGAA	GACGCAAAAG	ACAGGCAAGC	GCTCCACCAAG	CGCCGCGGTG	1560
306	CTGGAGGCC	TACGGGAGGC	CCACCCCATC	GTGGAGAAGA	TCCTCCAGCA	CCGGGAGCTC	1620
308	ACCAAGCTCA	AGAACACCTA	CGTGGACCCC	CTCCCAAGCC	TCGTCCACCC	GAGGACGGGC	1680
310	CGCCTCCACA	CCCGCTTCAA	CCAGACGGCC	ACGGCCACGG	GGAGGCTTAG	TAGCTCCGAC	1740
312	CCCAACCTGC	AGAACATCCC	CGTCCGCACC	CCCTTGGGCC	AGAGGATCCG	CCGGGCCTTC	1800
314	GTGGCCGAGG	CGGGTTGGGC	GTGGTGGCC	CTGGACTATA	GCCAGATAGA	GCTCCCGTC	1860
316	CTCGCCCACC	TCTCCGGGA	CGAAAACCTG	ATCAGGGTCT	TCCAGGAGGG	GAAGGACATC	1920
318	CACACCCAGA	CCGCAAGCTG	GATGTTCGGC	GTCCCCCGG	AGGCCGTGGA	CCCCCTGATG	1980
320	CGCCGGCGG	CCAAGACGGT	GAACCTCGGC	GTCCCTCATCG	GCATGTCCGC	CCATAGGCTC	2040
322	TCCCAGGAGC	TTGCCATCCC	CTACGAGGAG	GGGGTGGCCT	TTATAGAGGC	TACTTCCAAA	2100
324	GCTCCCCAA	GGTGCAGGCC	TGGATAGAAA	AGACCCCTGGA	GGAGGGGAGG	AAGCGGGGCT	2160
326	ACGTGGAAAC	CCTCTTCGGA	AGAAGGCGCT	ACGTGCCGA	CCTCAACGCC	CGGGTGAAGA	2220
328	GCGTCAGGGA	GGCCGCGGAG	CGCATGGCCT	TCAACATGCC	CGTCCAGGGC	ACCGCCGCCG	2280
330	ACCTCATGAA	GCTCGCCATG	GTGAAGCTCT	TCCCCCGCCT	CCGGGAGATG	GGGGCCCGCA	2340
332	TGCTCCTCCA	GGTCCACGAC	GAGCTCCTCC	TGGAGGCCCG	CCAAGCGCCG	GCCGAGGAGG	2400
334	TGGCGGCTTT	GGCCAAGGAG	GCCATGGAGA	AGGCCTATCC	CCTCGCCGTG	CCCCTGGAGG	2460
336	TGGAGGTGGG	GATGGGGAG	GACTGGCTT	CCGCCAAGGG	TTAG		2504

338 (2) INFORMATION FOR SEQ ID NO: 4:

340 (i) SEQUENCE CHARACTERISTICS:

341 (A) LENGTH: 832 amino acids

342 (B) TYPE: amino acid

343 (C) STRANDEDNESS: single

344 (D) TOPOLOGY: linear

346 (ii) MOLECULE TYPE: protein

350 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

352 Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu

RAW SEQUENCE LISTING
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353	1	5	10	15
355	Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly			
356	20	25	30	
358	Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala			
359	35	40	45	
361	Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val			
362	50	55	60	
364	Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly			
365	65	70	75	80
367	Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu			
368	85	90	95	
370	Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu			
371	100	105	110	
373	Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys			
374	115	120	125	
376	Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp			
377	130	135	140	
379	Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly			
380	145	150	155	160
382	Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro			
383	165	170	175	
385	Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn			
386	180	185	190	
388	Leu Pro Gly Val Lys Glu Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu			
389	195	200	205	
391	Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu			
392	210	215	220	
394	Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys			
395	225	230	235	240
397	Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val			
398	245	250	255	
400	Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe			
401	260	265	270	
403	Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu			
404	275	280	285	
406	Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly			
407	290	295	300	
409	Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp			
410	305	310	315	320
412	Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro			
413	325	330	335	
415	Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu			
416	340	345	350	
418	Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro			
419	355	360	365	
421	Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn			
422	370	375	380	
424	Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu			
425	385	390	395	400